CLAIMS:

1. An *in vitro* method for diagnosing or detecting a predisposition to a disease or disorder associated with abnormal RANTES gene expression, the method comprising examining the RANTES gene promoter to detect the presence of a genetic polymorphism.

2. A method as claimed in claim 1 carried out on genomic DNA.

3. A method as claimed in claim 2 in which the genomic DNA is isolated from blood or tissue samples or from other suitable sources.

4. A method as claimed in any preceding claim in which a region around –400 of the RANTES gene promoter relative to the transcription start site of Nelson *et al.* is examined to detect the presence of a genetic polymorphism.

5. A method as claimed in claim 4 in which the –400 base of the RANTES gene promoter is examined to detect the presence of a genetic polymorphism from Guanine (G) to Adenine (A).

6. A method as claimed in any one of claims 1 to 3 in which a region around –28 of the RANTES gene promoter relative to the transcription start site of Nelson *et al.* is examined to detect the presence of a genetic polymorphism.

7. A method as claimed in claim 6 in which the –28 base of the RANTES gene promoter is examined to detect the presence of a genetic polymorphism from Cytosine (C) to Guanine (G).

8. A method as claimed in any one of claims 4 to 7 in which the presence of a genetic polymorphism in the RANTES gene promoter is determined by nucleic acid

techniques based on size or sequence, such as hybridisation techniques, nucleic acid sequencing or restriction fragment length polymorphism.

9. A method as claimed in claim 8 in which the presence of a genetic polymorphism in the RANTES gene promoter involves amplification by polymerase chain reaction (PCR) of at least a fragment of the DNA with suitable PCR primers.

10. A method as claimed in claim 9 in which the DNA is subjected to PCR amplification using PCR primers specific for the region around the polymorphic site only.

11. A method as claimed in claim 10 in which the DNA is subjected to PCR amplification using PCR primers specific for a fragment of DNA of under 200 bases.

12. A method as claimed in claim 11 in which PCR primers suitable for amplifying a region around the –400 polymorphism relative to the transcription start site of Nelson *et al*. are listed below as SEQ ID No. 1 and SEQ ID No. 2.

Forward primer: 5' GCC TCA ATT TAC AGT GTG 3' (SEQ ID No. 1)
Reverse primer: 5' TGC TTA TTC ATT ACA GAT GTT 3' (SEQ ID No. 2)

13. A method as claimed in claim 11 in which PCR primers suitable for amplifying a region around the –28 polymorphism relative to the transcription start site of Nelson *et al*. are listed below as SEQ ID No. 3 and SEQ ID No. 4.

Forward primer: 5' ACA GAG ACT CGA ATT TCC GGA 3' (SEQ ID No. 3)
Reverse primer: 5' CCA CGT GCT GTC TTG ATC CTC 3' (SEQ ID No. 4)

14. A method according to any one of claims 8 to 13 further comprising the step of analysing the amplification product by restriction digestion and size analysis.

15. A method of treatment for individuals who either have or are predisposed to diseases or disorders associated with abnormal RANTES gene expression by administering to individuals who have a RANTES promoter polymorphism, as determined by the method according to claim 1, a modulator of RANTES activity.

16. A method as claimed in claim 15 in which the RANTES modulator is an enhancer of RANTES activity.

17. A method as claimed in claim 15 in which the RANTES modulator reduces the activity of RANTES.

18. Use of a method according to any one of claims 1 to 14 for diagnosing of patients with, or having a predisposition to developing, inflammatory diseases.

19. Use of a method according to any one of claims 1 to 14 for diagnosing of patients with, or having a predisposition to developing, asthma.

20. Use of a method according to any one of claims 1 to 14 to indicate those individuals having protection from HIV infection.